**IN THE SPECIFICATION:**

Page 6, after the first full paragraph, please insert the following:

The present invention concerns a protein that comprises the sequence SEQ ID NO: 1 but has a substitution(s) at positions 54 and/or 104 of SEQ ID NO: 1. The region corresponding to SEQ ID NO: 1 in the protein may comprise further changes (deletions and/or substitutions and/or additions). Thus the protein will comprise a region which is homologous to SEQ ID NO: 1. Preferably proteins of the invention comprising such homologous regions will retain reductase activity.

The homologous sequence typically has at least 70% homology, preferably at least 80%, 90%, 95%, 97% or 99% homology, for example over a region of at least 30, 100, 200 or more contiguous amino acids, such as over the entire length of SEQ ID NO: 1. The homology may be calculated on the basis of amino acid identity (sometimes referred to as "hard homology").

For example the UWGCG Package provides the BESTFIT program which can be used to calculate homology (for example used on its default settings) (*Devereux el al* (1984) *Nucleic Acids Research* **12**, p387-395). The PILEUP and BLAST algorithms can be used to calculate homology or line up sequences (such as identifying equivalent or corresponding sequences (typically on their default settings)), for example as described in Altschul S. F. (1993) J Mol Evol 3 6:290-300; Altschul, S, F et al (1990). J Mol Biol 215:403-10.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves

first identifying high scoring sequence pair (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighbourhood word score threshold (Altschul *et al*, supra). These initial neighbourhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extensions for the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the. sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) *Proc, Natl. Acad. Sci.* USA 89: 10915-10919) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

The BLAST algorithm performs a statistical analysis of the similarity between two sequences; *see e.g.*, Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90: 5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two amino acid sequences would occur by chance, For example, a sequence is considered similar to another sequence if the smallest sum probability in comparison of the first sequence to the second

sequence is less than about 1, preferably less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

The homologous sequence typically differs from SEQ ID NO: 1 by less than 100 mutations, such as less than 70, less than 50, less than 30 or less than 15 mutations (each of which may be a substitution, deletion or addition of an amino acid).